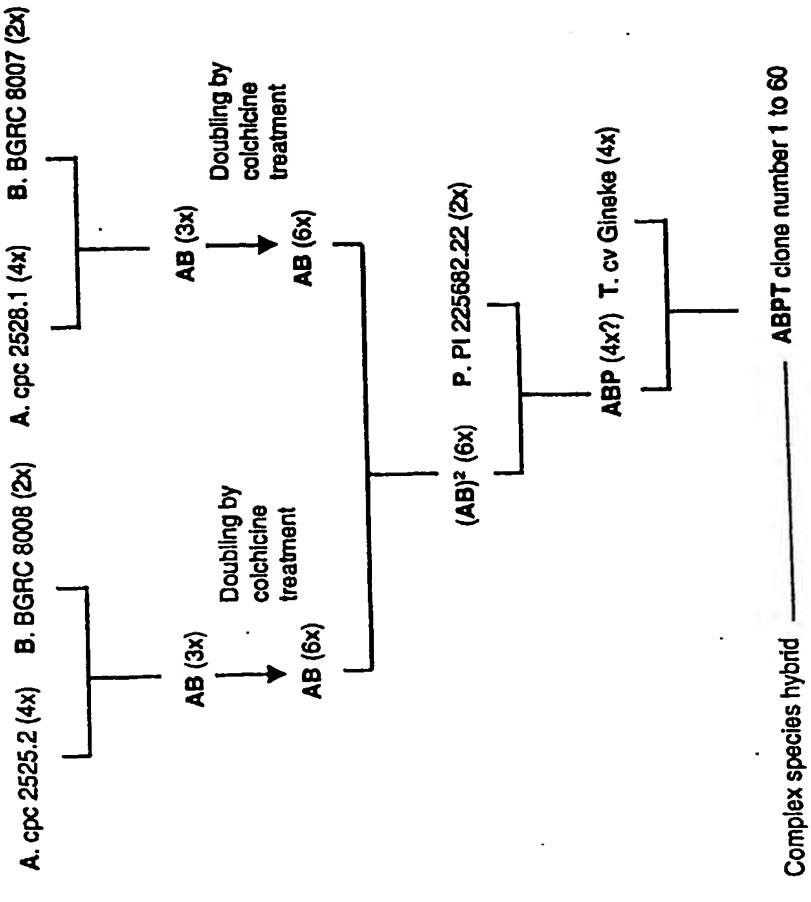


Figure 1A

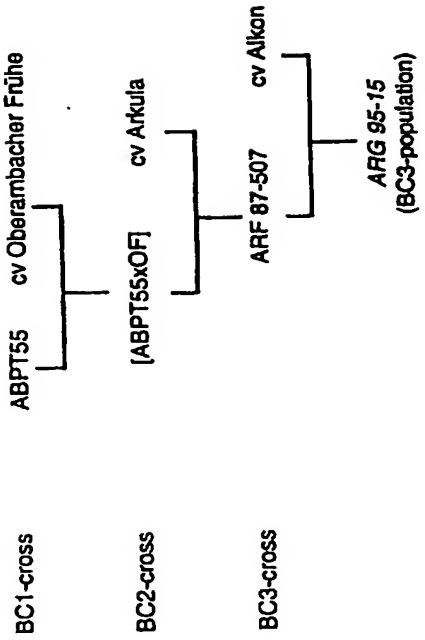

BC1-cross
BC2-cross
BC3-cross
ABPT55
cv Oberambacher Frühe
[ABPT55xOF]
cv Arkula
ARF 87-507
cv Alkon
ARG 95-15
(BC3-population)

Figure 1B

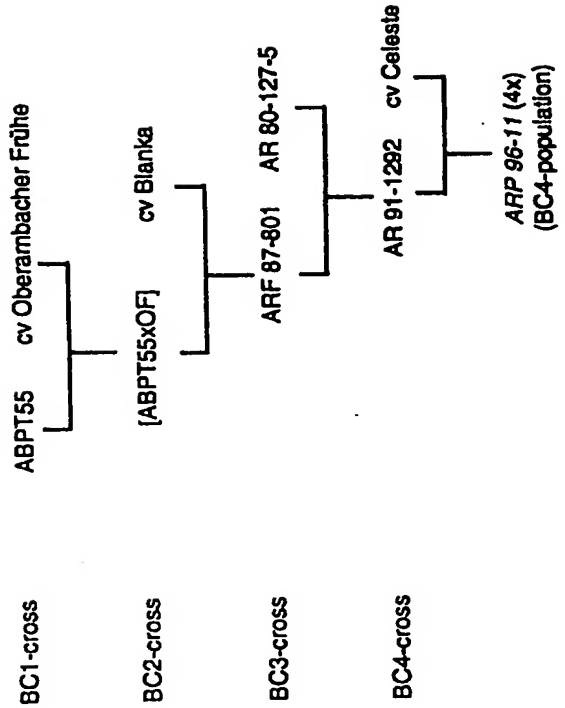

BC1-cross
BC2-cross
BC3-cross
BC4-cross
ABPT55
cv Oberambacher Frühe
[ABPT55xOF]
cv Blanka
ARF 87-801
AR 80-127-5
AR 91-1292
cv Celeste
ARP 96-11 (4x)
(BC4-population)

Figure 1C

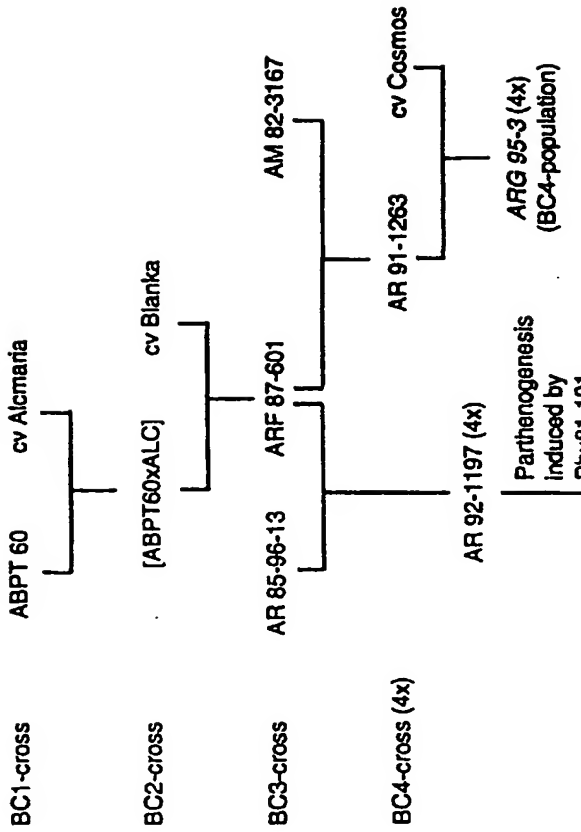

BC1-cross
ABPT 60
cv Alcmaria
BC2-cross
[ABPT60xALC]
cv Blanka
BC3-cross
AR 85-96-13
ARF 87-601
AM 82-3167
BC4-cross (4x)
AR 91-1263
cv Cosmos
AR 92-1197 (4x)
Parthenogenesis induced by Phu81-101
ARG 95-3 (4x) (BC4-population)
BC4-cross (2x)
ARD 1197-16 (2x)
ARD 93-2090 (2x)
DP1 (2x) (BC4-population)

Figure 1D

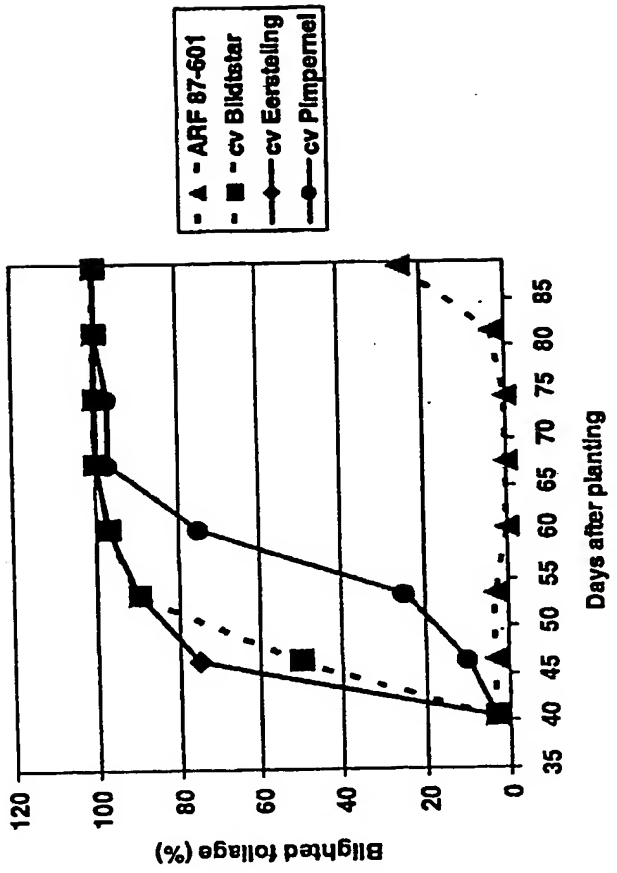

- ▲ - ARF 87-601
- ■ - cv Bildstar
cv Eersteling
cv Pimpernel
Blighted foliage (%)
120
100
80
60
40
20
0
35 40 45 50 55 60 65 70 75 80 85
Days after planting

Figure 2

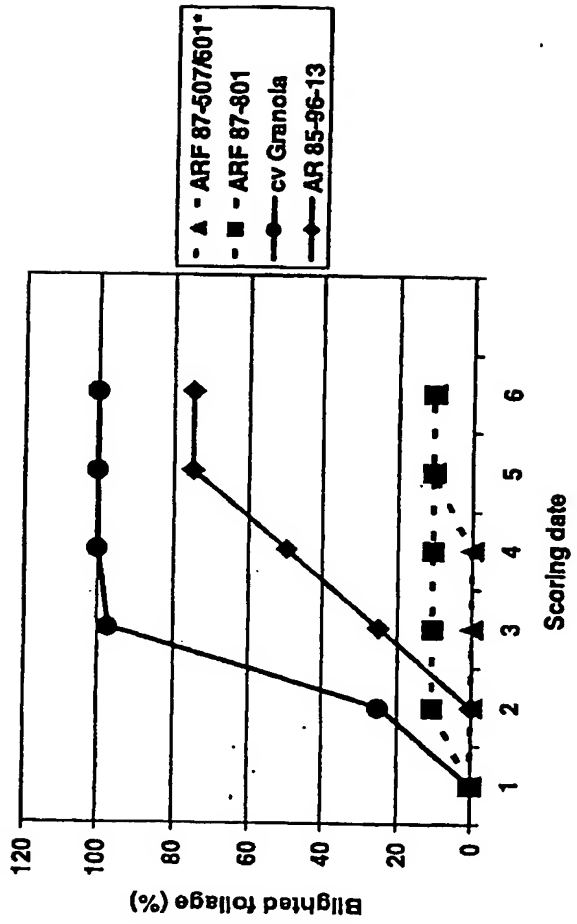


Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves

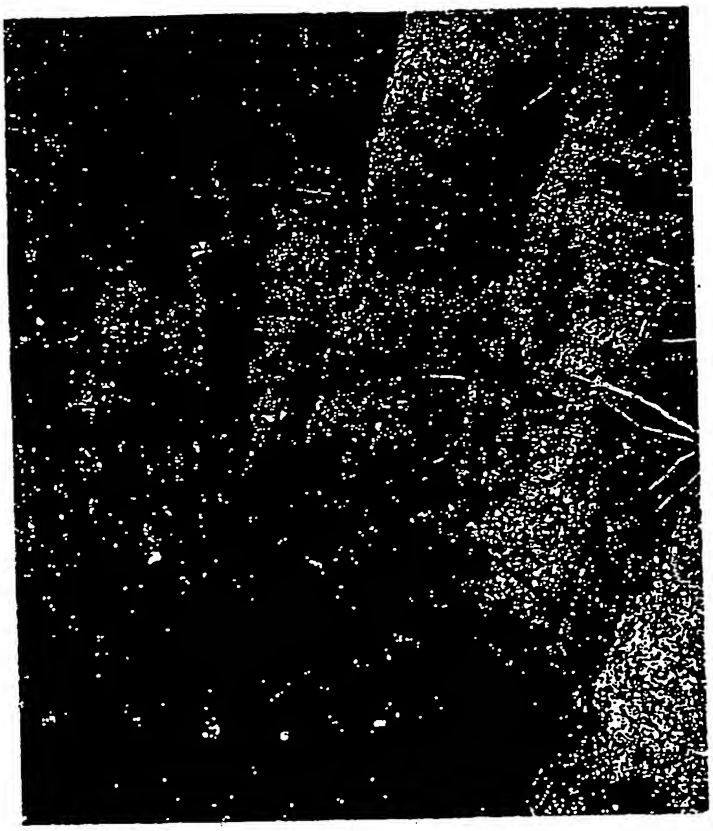


Figure 4

Figure 4 dia 3

Figure 4 dia 4

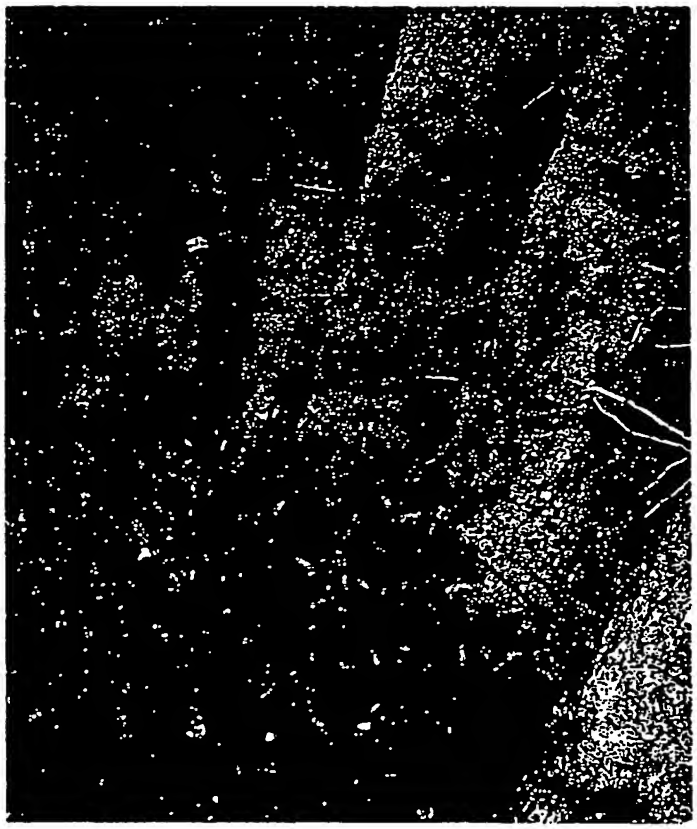
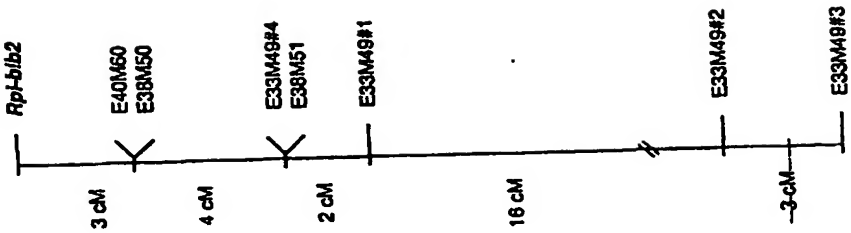


Figure 4 dia 5

Figure 4 dia 6



ARG 95-15

Figure 5

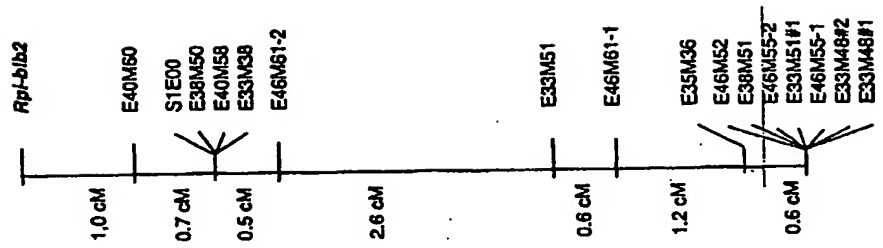

Rpi-blb2
E40M60
S1E00
E38M50
E40M58
E33M38
E46M61-2
E33M51
E46M61-1
E35M36
E46M52
E38M51
E46M55-2
E33M51#1
E46M55-1
E33M48#2
E33M48#1
1,0 cM
0.7 cM
0.5 cM
2.6 cM
0.6 cM
1.2 cM
0.6 cM
ARG 95-3

Figure 6

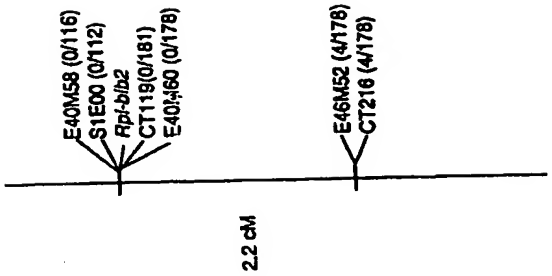
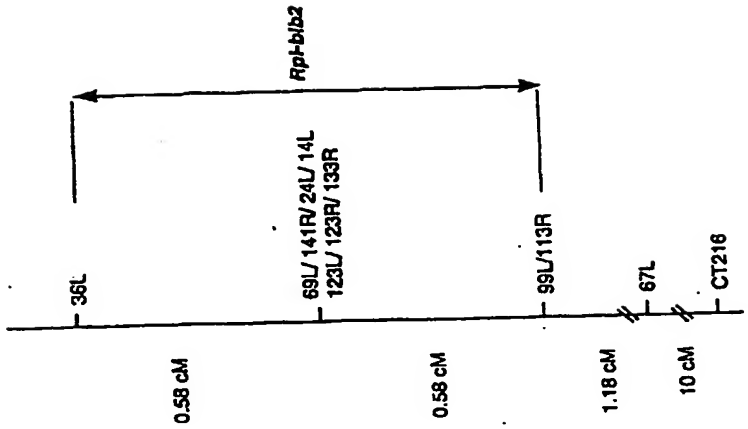
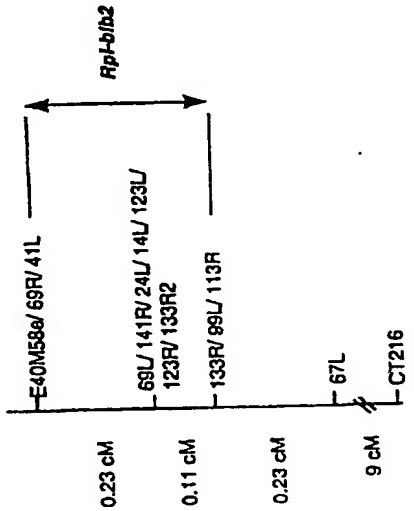

E40M58 (0/116)
S1E00 (0/112)
Rpi-blb2
CT119(0/181)
E40I60 (0/178)
E46M52 (4/178)
CT216 (4/178)
2.2 cM
ARG 95-3

Figure 7



ARP 96-11



ARG 95-3

Figure 8

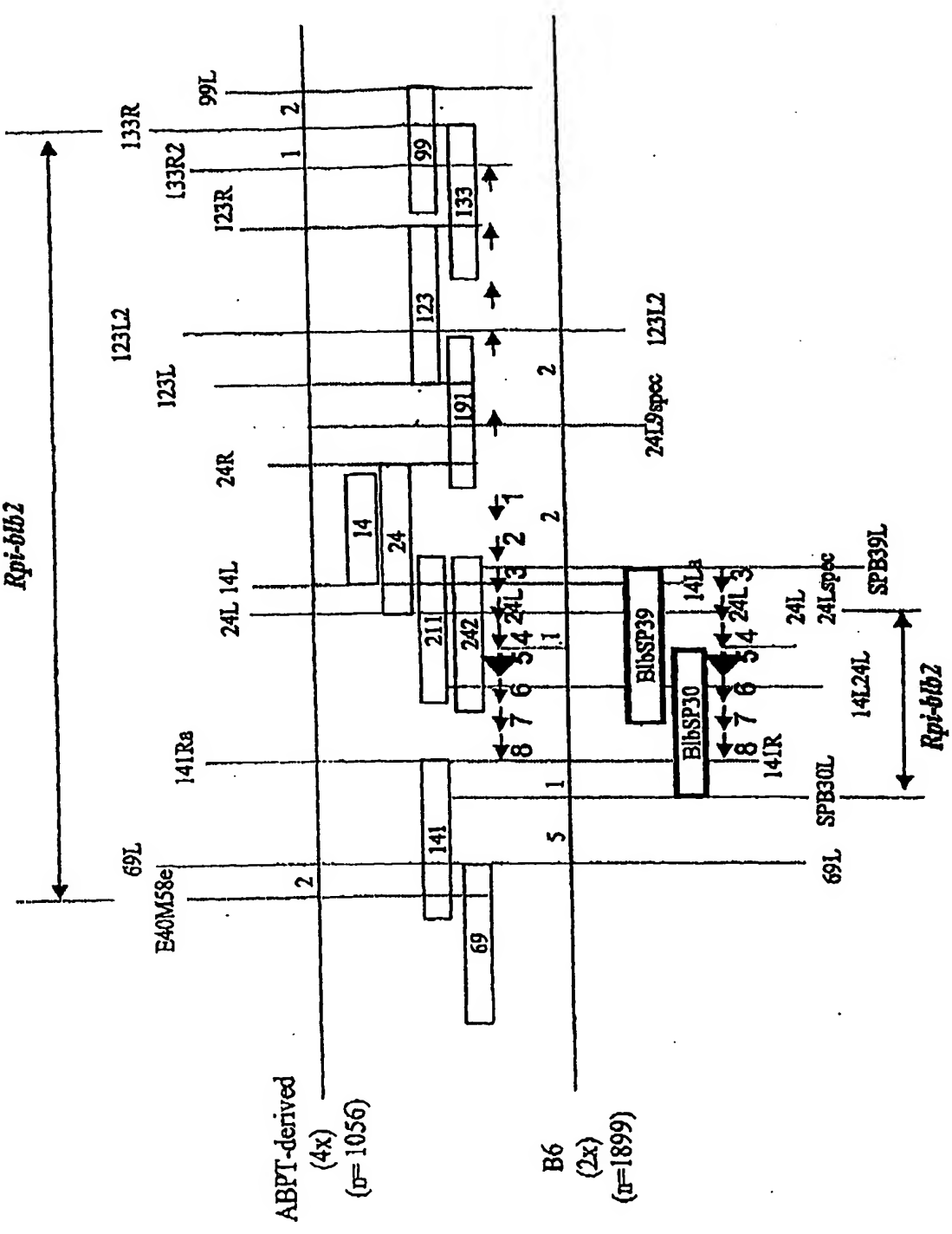

Rpi-blb2
69L
E40M58e
141Rs
24L 14L
24R
123L
123L2
133R2
133R
99L
ABPT-derived
(4x)
(n= 1056)
B6
(2x)
(n=1899)
BlbSP39
BlbSP30
14L24L
Rpi-blb2

Figure 9

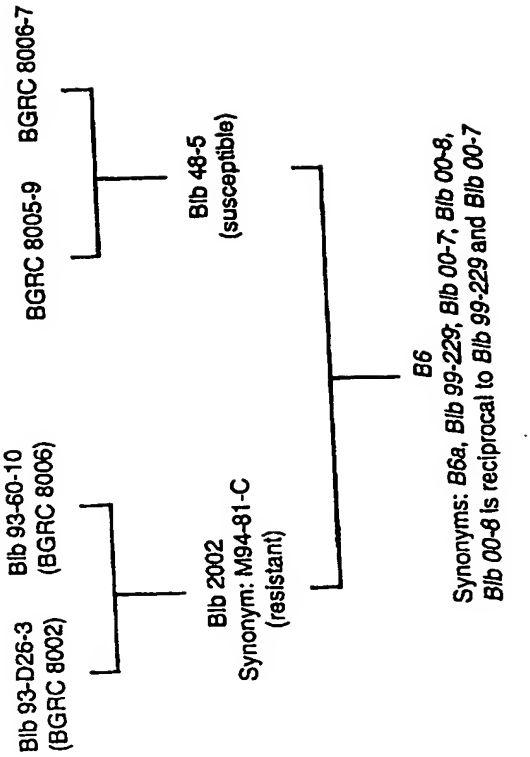

B6
Synonyms: B6a, Blb 99-229; Blb 00-7; Blb 00-8,
Blb 00-8 is reciprocal to Blb 99-229 and Blb 00-7
Blb 2002
Synonym: M94-81-C
(resistant)
Blb 48-5
(susceptible)
BGRC 8005-9
BGRC 8006-7
Blb 93-60-10
(BGRC 8006)
Blb 93-D26-3
(BGRC 8002)

Figure 10

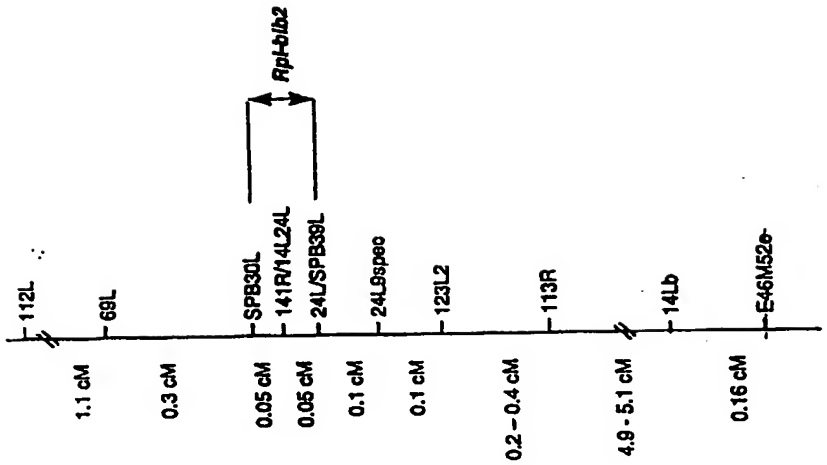

Rpl-b/b2
112L
69L
SPB30L
141R/14L24L
24L/SPB39L
24L9spec
123L2
113R
14Lb
E46M52e
1.1 cM
0.3 cM
0.05 cM
0.05 cM
0.1 cM
0.1 cM
0.2 – 0.4 cM
4.9 - 5.1 cM
0.16 cM
B6

Figure 11

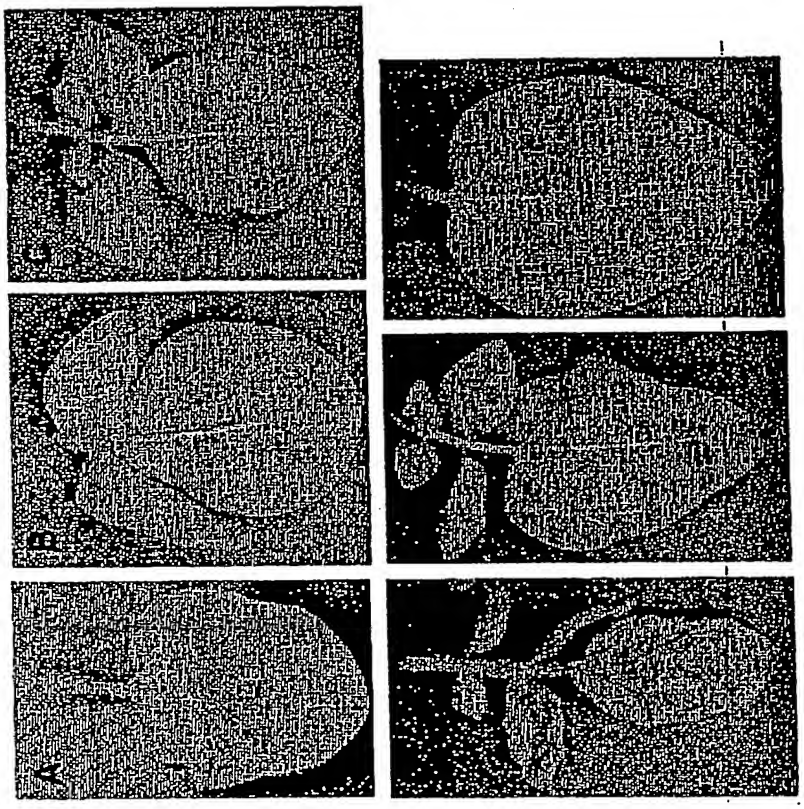


Figure 12

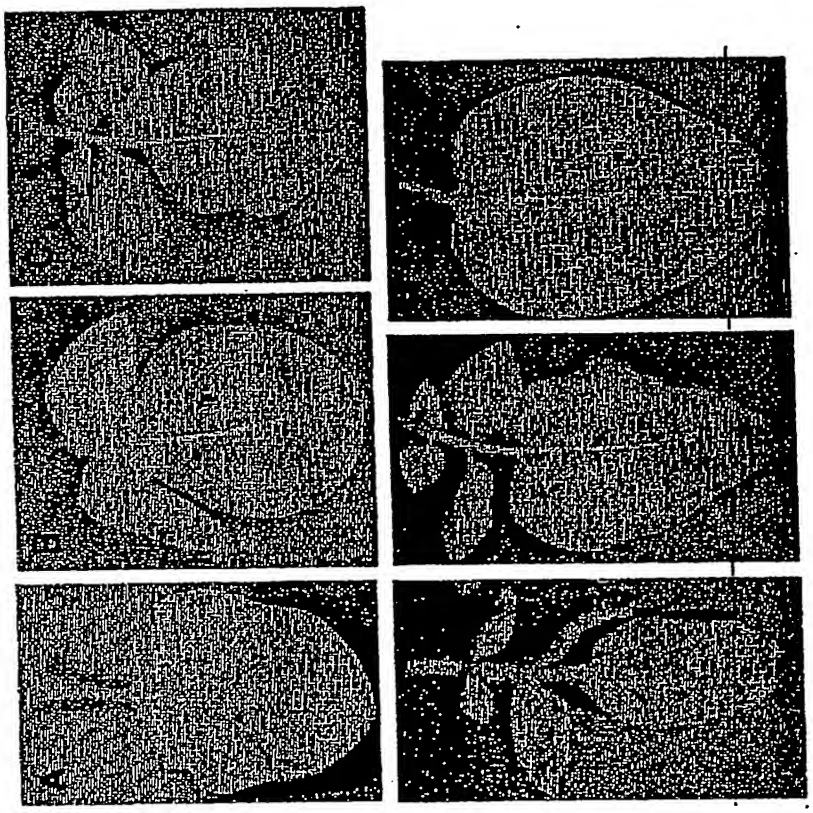


Figure 12 dia2

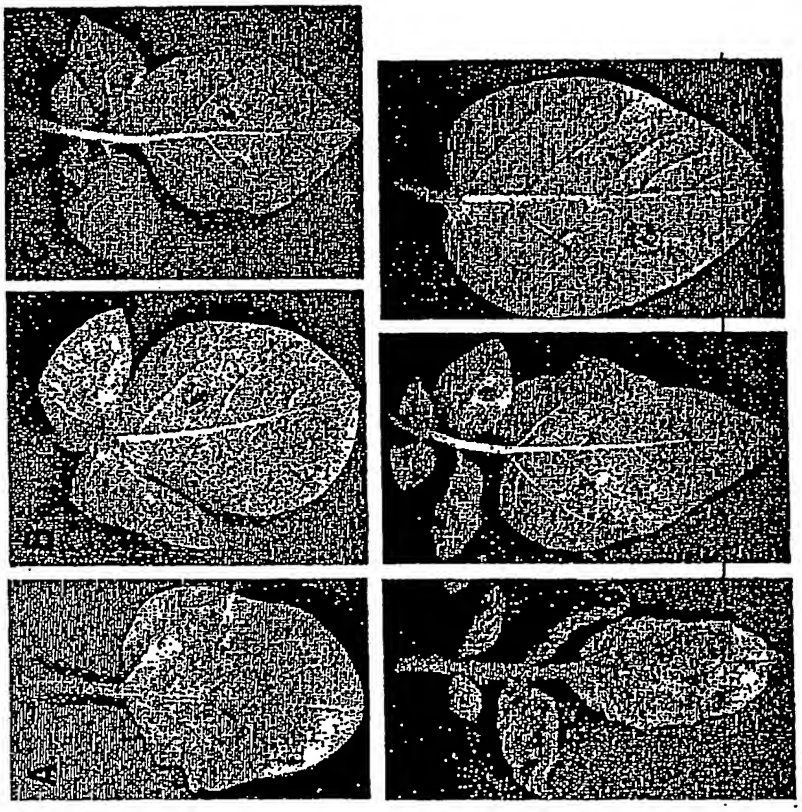


Figure 12 dia 3

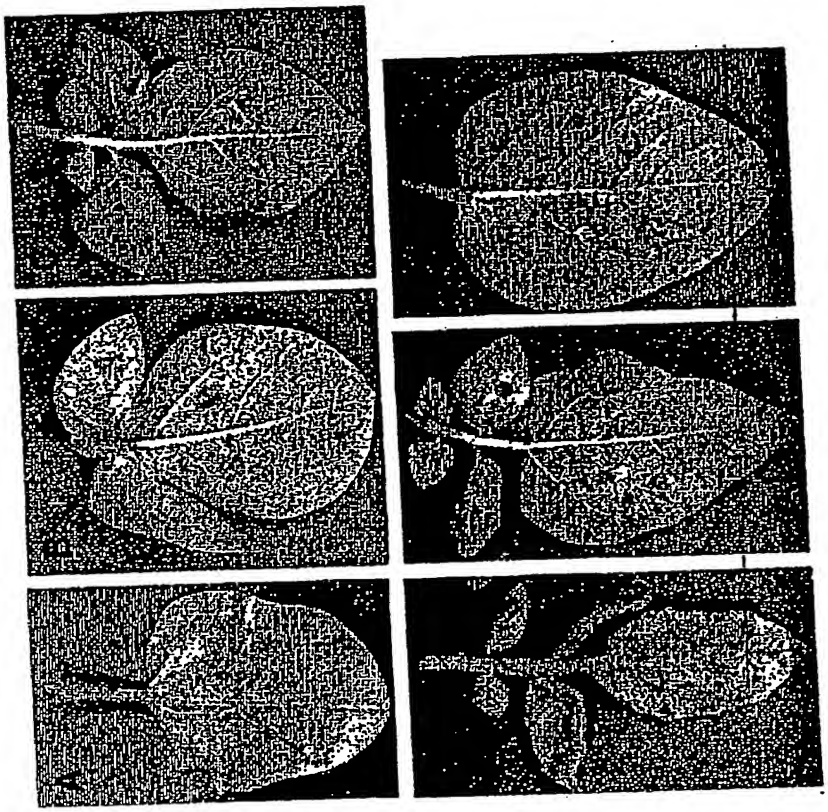


Figure 12 dia 4

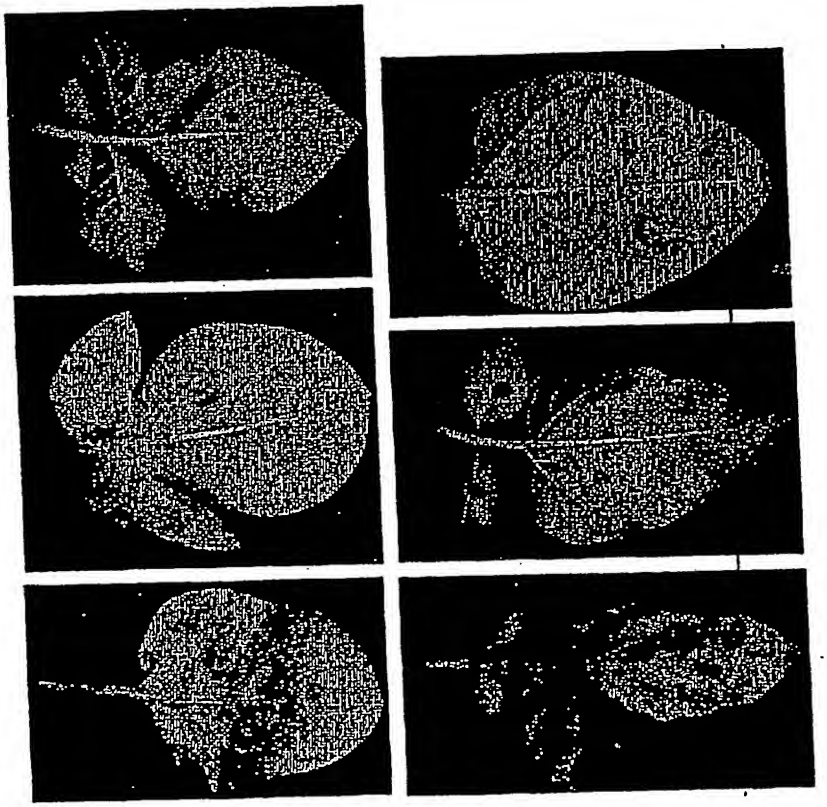


Figure 12 dia 5

Figure 13A

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TTCTGCTCTTCGCAAGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGAT 100
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CTGAAATTGAAGCTGACATTTATTTGTACATATGTCCAGCTTTCTTATTC 200
CGATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTG 250
AGAATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGT 300
AAATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTT 350
GTATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCT 400
TCCTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATG 450
TTTCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACAT 500
AAGAGATTTCCATGGATTGATAGTGAATTGTTGCATTAAGCATGAGATGG 550
TTGAGAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGC 600
TTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGA 650
TGAGGATGATCAGAATGATAAAGACCCTCAACTCTTCAAGCTAGCACATC 700
TACTCTTGAAGATTGTTCCAACTGAATTGGAGGTTATGCACATATGTTAT 750
AAAACTTTGAAAGCTTCAACTTCAACAGAAATTGGACGCTTCATTAAGAA 800
GCTCCTGGAAACCTCTCCGGACATTCTCAGAGAATATCTGATTCATCTAC 850
AAGAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGAAAC 900
ATTCATGTCATGATGGAATTCCTATTGATTATTCTTTCTGATATGCCGCC 950
CAAGGACTTTATTCATCATGACAAACTTTTTGATCTCTTGGCTCGTGTTG 100
TAGCACTTACCAGGGAGGTATCAACTCTTGTACGCGACTTGGAAGAGAAA 1050
TTAAGGATTAAAGAGAGTACTGACGAAACAAATTGTGCAACCCTAAAGTT 1100
TCTGGAAAATATTGAACTCCTTAAGGAAGATCTCAAACATGTTTATCTGA 1150
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TTCATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCAATGC 1250
TTATTCAATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACT 1300
TGGAATTCATAAGATCTTTTTTCGCGAATATTGAGCAAGGATTGTATAAA 1350
GATCTCTGGGAACGTGTTCTAGATGTGGCATATGAGGCAAAAGATGTCAT 1400
AGATTCAATTATTGTTCGAGATAATGGTCTCTTACATCTTATTTTCTCAC 1450
TTCCCATTACCAGAAAGAAGATGATGCTTATCAAAGAAGAGGTCTCTGAT 1500
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CAAGAAACCAGTTGAGAGCAAGTCATTGACAACTGATAAAATAATTGTAG 1600
GTTTTGGTGAGGAGACAAACTTGATACTTAGAAAGCTCACCAGTGGACCG 1650

GCAGATCTAGATGTCATTTCGATCATTGGTATGCCGGGTTTAGGTAAAAC 1700
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ACCTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAGAAGTTG 1800
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ATCTTATTGTCTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTA 1950
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GCCATGGGATTTTCACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATG 3400

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AACTTGAAAATTCCGCTCTCAAGATTAAGGAATATGCTGAAGATATGAGG 3750
GGAGGGGACGAGCTTCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAA 3800
GTAG 3804

Figure 13B

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*AAAAATTTGATATGTGTTATTTTGGCAG*GAGTCATTTTCTGCTCTTCGCA 150
AGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGATTAAAGAATGAAGAA 2001
GATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTGAAGCT 2501
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TCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGCTTCCTTTGGGAGGA 7001
TCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGATGATCAGA 7501
ATGATAAAGACCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATT 8001
GTTCCAACTGAATTGGAGGTTATGCACATATGTTATAAAACTTTGAAAGC 8501
TTCAACTTCAACAGAAATTGGACGCTTCATTAAGAAGCTCCTGGAAACCT 9010
CTCCGGACATTCTCAGAGAATATCTGATTCATCTACAAGAGCATATGATA 9510
ACTGTTATTACCCCTAACACTTCAGGGGCTCGAAACATTCATGTCATGAT 1000
GGAATTCCTATTGATTATTCTTTCTGATATGCCGCCCAAGGACTTTATTC 1050
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GATGACGTGTGGGATACTAATACATGGGATGAGCTAACAAGACCTTTTCC 2050
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TTGCTTTGCATGGAAAGCTCTACACTGATCCTCTTAACCTTCGATTGCTA 2150
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CAGAAGTTAAATCTCTGCCTTTGTCTTTCTCAAACCTCTGGAATCTAGAA 3050
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GTCGGACTGTCATAATCTTGAGGAGATTCCGTCTAGTTTTGGGGATATTT 3750
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GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGGACGAGCT 3850
TCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAAGTAG 3890

Figure 13C

GATCTAGAATCACCGAACCTCCCCTCGGTACAGCTCCTCCAGTTCTACCA 50
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TCTATGCTCAAAAAATCCCGAGATAAAACCCTAGATCTGCTTCAAATGCT 150
CTGATACCATGTAATTTCAGTGAATTCTAACTAAACAATGGAGAGAATTA 200
ACTATTTTAGAAAGACTGATTGAAGGAGAAGAAGAGAGAAAAATTCTATA 250
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Figure 13D

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GCCCACATAAAAAAAATGAAATATTACAAAAACCCTGATAATAAAATACAC 7700
TAATCTAAGATATTCACTGCAACATACATGCAAAATATATATATATAAAT 7750
TTTCATGAAAATTATAACAAATAATAGATGTGAACATATAACTTTAAAAA 7800
TAATATTACATCCATAAAGCTTAAATTCTAGATCCATCTATGCTTGTATG 7850
ATGCATAGCTCAGAATATCTCCATCAAGTGTTAAACTACATATTTCATTC 7900
AAATTTATATAGAAAACGATAATTAAGGTGAAAACTTTTATAAAGATATC 7950
GTGTGGTTGTGTGAGTGAGGTGACAAAATAAGTTGTGTGATTATTCAAAA 8000
AGTTTTAATAACGAAAATCCACATGCTTGAATTAATTGAAGCATTAATGT 8050
TGTAACGAAAAATATTACATTTATTGAGTTACTGTGATGTTTTAACTGAT 8100
ATATAAAATAATATTGGTATTTCTCTTCATCTGCGACATAATATGTTTTT 8150
TCATCTTTTTTCAATATACAAAATAGAATTATTATTTTGTTGCATCTTTT 8200
TAAGTACAAATTATTCATATGTATATAGTACAAAATAAAATATTTACTGT 8250
GGTAAAGTAAATGGAATAAGAGGTCATATTTGAAATAACAATATACTATA 8300
CTATGTTAAAGTATTTTTTATAGTTAAAATTTCTCTAGAGTACTTGATTC 8350
TACATACAAATACTAATTTCGTAAAAAAATTAATATTGAATTTCTTCATT 8400
GTTTCTTTATTATTAAATTAGTTTATAATAACTAAACTAAGGTAATAAGA 8450
CCTTAGTTTAGTTAATGTGTGTCTCTGTGATTTCGTTCATAGTCTAAGGG 8500
TGTACTTGTGCCTTATCCCAAAAATGAAGGAATATCAAAAGATATATTAA 8550
AATTAAATTAAATATTTGGAGGTTATGAATATAAAAAGTATCAGAGTTCT 8600
ACATATAAAGAGTAACAATTGAAATAATTAATTAAATATGAGATATGAAG 8650

GCGGACATTTAAAGAAAATAATAAATAAATAAATTAAAGGGTATAAATTT 8700
CATAATACATAATACCAATAAGCCGTAGAATATCTCCGTCATAATGCATA 8750
AACTAATAAATCACAAATGTATAACTCACATACAAATATTTTTTGATAAA 8800
GAATTTGAATGTTGTAATAGAATGGAGAATAACTTGTGTCTTATTCCATT 8850
ATGTAAGACGTATAAATACAAATACAATGAGCTCTAATTAATTAAGGAAA 8900
CTAAATAAGGAAGGAATCAAAAAATATTATGTCATATCCCTACATATCTG 8950
CTAGAGATTCTATCATATCCTTACATATCTGTTAAGCTATGTCTACACCT 9000
AAAGGTGTCTACAATCATTTTGTAACACTCCCCCTCAAGTTAGAGCATAG 9050
ATATTATTCATTCCCAACTTGTTACAAAGATAATCAACTCGAGTTCCATT 9100
CAACGCTTTTGTGAACAAATCAACTAGTTGCTCTCCTGTCTTCACTTAGC 9150
TAGTGGATATCAGGTTTTCATGAATCTTCTCACGAATAAAATGACAGTCA 9200
ACCTCAATATGTTTAGTTCTTTCATGAGACACCGGATTCAAGGCAATATG 9250
GAGCGCAACTTGATTATCATACTAGAGTTTTGATGGTATATGATGCTTCA 9300
ACCCTATTTCTGTTAAAAGATAATGTATCCACATGATCTCACCCATAGAC 9350
TGTAACATAACTCTGTACTTTGATTCTGCACTAGATCAAGATACAACATT 9400
TTGCTTTTTACTCCTCCATGATACCAGGTTTCATCCAACAAAGACACAAT 9450
AACTTGTAGTAGATCTTCTATCAATTTTCGATCCAGCCCAATCGACATCT 9500
GCAAAACACTCAATATGAGTATGGTCGTGATTTTGATACTATATTCCAAG 9550
ACTAGGAGTTTTCTTCAAGTAACATAGAATATGTTCCAAAGCTGCCCAGT 9600
GTTTGACGTAGGTGCAAACATGAACTAGCTAACAACACTTACTGCAAAAG 9650
CAATATCAAGATGAGTCACAATAAGGTAGTTTAACTTTCCAACTAACCTT 9700
TTGTATCTCTATGGATCATTAAAAGGATCGTCGTCATCTTTCATAAGATG 9750
CATATTGGGAACCATTGGAGAACTTCAGGGTTTGGCTGCCATCTTTCAAT 9800
TTTCTGCAAGTAGATCGAGAGAATATATTCTCTAAGACAAAAGAATTCCC 9850
TTTTTGTTTCTATTTACTTCTACTCCCAAAATGTATTTCAATTGACCCAA 9900
GTCCTTCGTATGAAACCAAGTATGCAGGAAAGACTTGAGGGAAGAGATC 9949

A

B

LZ

MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIE
SLKLKLTFICTYVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDV
GCKYVLTSLAGNMDDCISLYHRSKSDATMMDEQLGFLLLNLSHLSKHRA
EKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCIKHEMVENVLSLFQLMAE
RVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIVPTELEV
MHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPN
TSGARNIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTL
VRDLEEKLRIKESTDETNCATLKFLENIELLKEDLKHVYLKVPDSSQYC
FPMSDGPLFMHLLQRHLDDLLDSNAYSIALIKEQIGLVKEDLEFIRSFF
ANIEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLLHLIFSLPITRKK
MMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEET

NBS

NLILRKLTSGPADLDVISII*gmpglgkttla*YKVYNDKSVSSHFDLRAW
CTVDQVYDEKKLLDKIFNQVSDSNSKLSENIDVADKLRKQLFG*kryliv*
*lddvwD*TNTWDELTRPFPDGMKG*sriilttr*EKKVALHGKLYTDPLNLR
LLRSEESWELLEKRAFGNESCPDELLDVGKEIAENCK*glplvvdliag*I
IAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH*lkpcll*
*yfas*APKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSS
LVICFNEIGDYPTCQ*l*hdl*v*hdFCLIKARKEKLCDRISSSAPSDLLPRQ
ISIDYDD

LRR

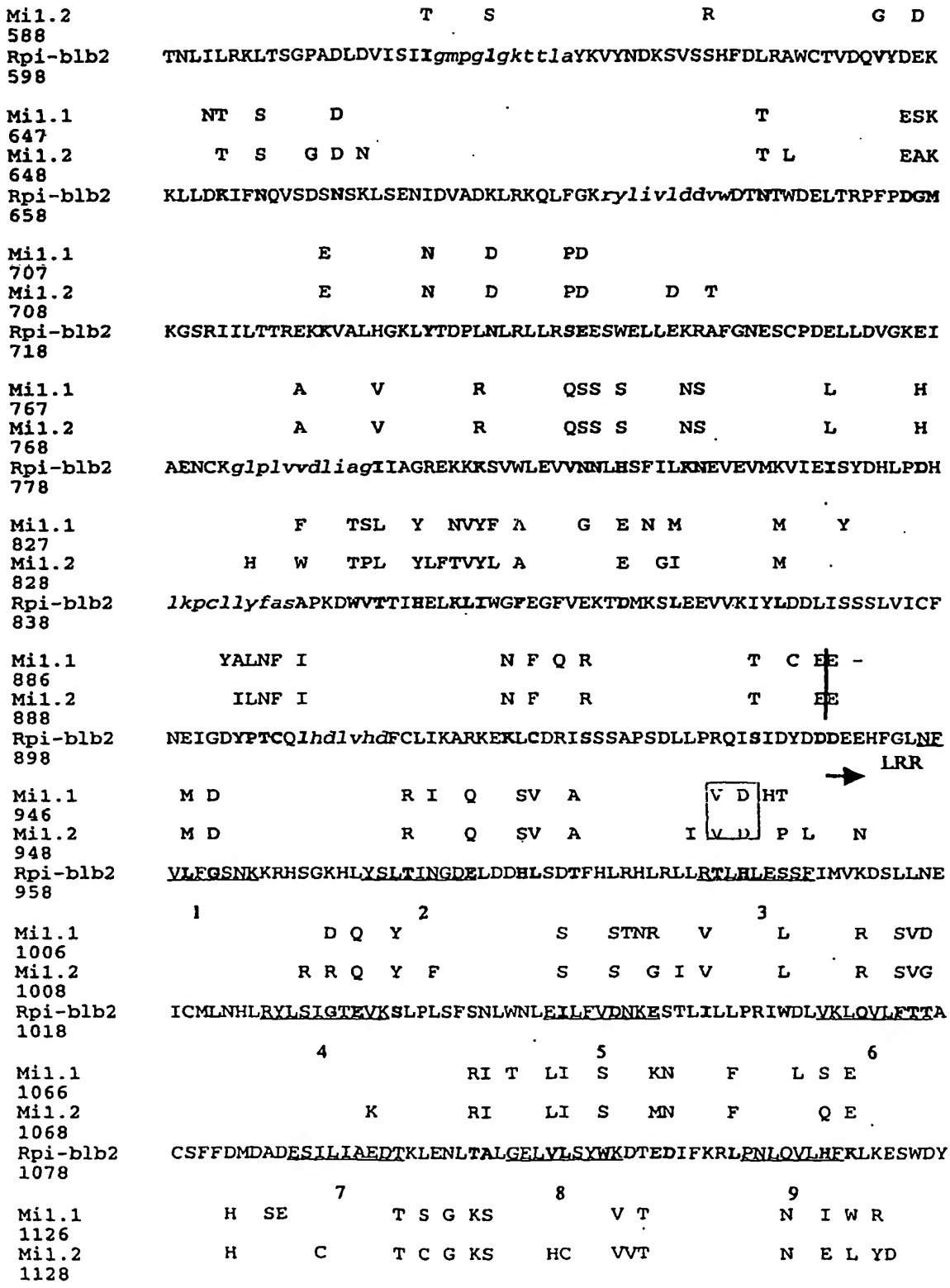
DEEHFGLNFVLFGSNKK	1
RHSGKHLYSLTINGDE.LDDHLSDTFH	2
LRHLRLLRTLHLESSFIMVKDSLLNE	3
ICMLNHLRYLSIGTEVKSLPLSF	4
SNBLWNLEILFVDNKESTLIL	5
LPRIWDLVKLQVLFTTACS	6
FFDMDADESILIAEDTK	7
LENLTALGELVLSYWKDT	8
EDIFKRLPNLQVLHFK.LKESWDYSTEQYWFPK	9
LDFLTELEKLTVDFERSNTNDSGSSAAINRPWD	10
FHFPSSLKRLQLHEFP.LTSDSLST	11
IARLLNLEELYLYRTI.IHGEEWNMGE	12
EDTFENLKCLMLSQVI.LSKWEVG	13
EESFPTLEKLELSDCHNLEEIPSS	14
FGDIYSLKIIELVRSPQLENSALK	15

IKEYAEDMRGGDELQILGQKDIPLFK

FIGURE 14

```
Mi1.1                    VL    S  I D  V   ---    N   L K QV KI    MA
57
Mi1.2             I      VL    S  I    I   ---    N   L K QV KL    MA
57
Rpi-blb2    MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT
60

Mi1.1            C  F Q  .               L    ---------F   TS
109.
Mi1.2            Y  F Q       N          SL   --------    TS
109
Rpi-blb2    YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR
120

Mi1.1        Y    I      D      Y     H   I            I             G
169
Mi1.2        Y    I      D      Y     H   I                        L G
169
Rpi-blb2    S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI
179

Mi1.1              P      D   H   D  T    R       E   R SR
229
Mi1.2              P          H       T    R       EH  R SR  Q T
229 Rpi-blb2
      KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239

Mi1.1        V    I    TN       A V L   Q              P      V      S
289
Mi1.2                   TN       A V                  I Q      L    P S L
289
Rpi-blb2    PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR
299

Mi1.1              L      -              D  GV               EP N  GNNQ
348
Mi1.2              L      -               H GT                  N  GNNQ
348
Rpi-blb2    NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE
359

Mi1.1              DL        K        AL    C              HI  N
408
Mi1.2              DL        K        A N   C              HM  N
408
Rpi-blb2    TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS
419

Mi1.1            E E   Q  K      VD-A         A
467
Mi1.2        S   E E  SQE        GDAA       I A
468
Rpi-blb2    IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL
478         ------------------

Mi1.1              I  IK     I A D   P D              R        T   E
527
Mi1.2              I  IK     I A D   P D              R        I   E
528
Rpi-blb2    HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE
538

Mi1.1                   S       T    S                 R          GC
587
```

FIGURE 15


Mi1.2 T S R G D
588
Rpi-blb2 TNLILRKLTSGPADLDVISIIgmpglgkttlaYKVYNDKSVSSHFDLRAWCTVDQVYDEK
598
Mi1.1 NT S D T ESK
647
Mi1.2 T S G D N T L EAK
648
Rpi-blb2 KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKrylivlddvwDTNTWDELTRPFPDGM
658
Mi1.1 E N D PD
707
Mi1.2 E N D PD D T
708
Rpi-blb2 KGSRIILTTREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCPDELLDVGKEI
718
Mi1.1 A V R QSS S NS L H
767
Mi1.2 A V R QSS S NS L H
768
Rpi-blb2 AENCKglplvvdliagIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH
778
Mi1.1 F TSL Y NVYF A G E N M M Y
827
Mi1.2 H W TPL YLFTVYL A E GI M
828
Rpi-blb2 lkpcllyfasAPKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF
838
Mi1.1 YALNF I N F Q R T C E E -
886
Mi1.2 ILNF I N F R T E E
888
Rpi-blb2 NEIGDYPTCQlhdlvhdFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF
898
LRR
Mi1.1 M D R I Q SV A V D HT
946
Mi1.2 M D R Q SV A I V D P L N
948
Rpi-blb2 VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE
958
1 2 3
Mi1.1 D Q Y S STNR V L R SVD
1006
Mi1.2 R R Q Y F S S G I V L R SVG
1008
Rpi-blb2 ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA
1018
4 5 6
Mi1.1 RI T LI S KN F L S E
1066
Mi1.2 K RI LI S MN F Q E
1068
Rpi-blb2 CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY
1078
7 8 9
Mi1.1 H SE T S G KS V T N I W R
1126
Mi1.2 H C T C G KS HC VVT N E L YD
1128

```
Rpi-blb2    STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT
1138
                                  10                                  11
Mi1.1                  P     S  H                   F NFN  SI
1186
Mi1.2                  P   N S  D   Q                F N RLLT
1188
Rpi-blb2    SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP
1198
                              12                            13
Mi1.1       N    K RG  K     P          S KI K     D
1246
Mi1.2       N    K QE GK     P          F KI K     D       K         ND
1248
Rpi-blb2    TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL
1258
                 14                          15
Mi1.1          N       1255
Mi1.2          N       1257
Rpi-blb2    GQKDIPLFK 1267
```

Figure 16: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 nucleic acids

```
CLUSTAL W (1.82) Multiple Sequence Alignments


Sequence format is Pearson
Sequence 1: Mi1.1          3768 bp
Sequence 2: Mi1.2          3774 bp
Sequence 3: Rpi-blb2       3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  95
Sequences (1:3) Aligned. Score:  89
Sequences (2:3) Aligned. Score:  89
Guide tree        file created:   [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:   2      Score:68908
Group 2: Sequences:   3      Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created  [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-
14435620.aln]


CLUSTAL W (1.82) multiple sequence alignment
```

Figure 17: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1 1255 aa
Sequence 2: Mi1.2 1257 aa
Sequence 3: Rpi-blb2 1267 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14322840.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score:25939
Group 2: Sequences: 3 Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14322840.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mi1.1 MEKRKDNEEANNSLVLFSALSKDIADVLVFLE---NEENQKALDKDQVEKIKLKMAFICT 57

```
Mi1.2          MEKRKDIEEANNSLVLFSALSKDIANVLIFLE---NEENQKALDKDQVEKLKLKMAFICT 57
Rpi-blb2       MEKRKDNEEANNSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFICT 60
               ****** *******  **** ** *:** ***   ***:***:* * :*.:***::****

Mi1.1          YVQLSCSDFEQFEDIMTRKRQEVENLLQPLLDDD--------VFTSLTSNMDDCISLYHR 109
Mi1.2          YVQLSYSDFEQFEDIMTRNRQEVENLLQSLLDDD--------VLTSLTSNMDDCISLYHR 109
Rpi-blb2       YVQLSYSDLEKFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR 120
               ***** **:*:*******:*********.:****        *:***:.**********

Mi1.1          SYKSDAIMMDEQLDFLLLNLYHLSKHHAEKIFPGVTQYEVLQNICGNIRDFHGLIVNGCI 169
Mi1.2          SYKSDAIMMDEQLDFLLLNLYHLSKHHAEKIFPGVTQYEVLQNVCGNIRDFHGLILNGCI 169
Rpi-blb2       S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI 179
               * **** ******.****** *****:***:***********:**********:* **

Mi1.1          KHEMVENVLPLFQLMADRVGHFLWDDQTDEDSRLSELDEDEQNDRDSRLFKLAHLLLKIV 229
Mi1.2          KHEMVENVLPLFQLMAERVGHFLWEDQTDEDSRLSELDEDEHNDRDSRLFQLTHLLLKIV 229
Rpi-blb2       KHEMVENVLSLFQLMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239
               *********.******:***:***:**:****:*******::**:*.:**:*:********

Mi1.1          PVELEVIHICYTNLKASTSAEVGLFIKQLLETSPDILREYLIPLQEHMVTVITPSTSGAR 289
Mi1.2          PTELEVMHICYTNLKASTSAEVGRFIKKLLETSPDILREYIIQLQEHMLTVIPPSTLGAR 289
Rpi-blb2       PTELEVMHICYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMITVITPNTSGAR 299
               *.****:****..******:*:* ***:************:* *****:***.*.* ***

Mi1.1          NIHVMMEFLLLILSDMP-KDFIHHDKLFDLLDRVGVLTREVSTLVRDLEEEPRNKEGNNQ 348
Mi1.2          NIHVMMEFLLLILSDMP-KDFIHHDKLFDLLAHVGTLTREVSTLVRDLEEKLRNKEGNNQ 348
Rpi-blb2       NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE 359
               **********:****** ************* :* .**************: * **..::

Mi1.1          TNCATLDLLENIELLKKDLKHVYLKALDSSQCCFPMSDGPLFMHLLHIHLNDLLDSNAYS 408
Mi1.2          TNCATLDLLENIELLKKDLKHVYLKAPNSSQCCFPMSDGPLFMHLLHMHLNDLLDSNAYS 408
```

```
Rpi-blb2        TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDDLLDSNAYS 419
                ******.:********:********. :*** **************: **:*********

Mi1.1           IALIKEEIELVKQDLKFIRSFFVD-AEQGLYKDLWARVLDVAYEAKDVIDSIIVRDNGLL 467
Mi1.2           ISLIKEEIELVSQELEFIRSFFGDAAEQGLYKDIWARVLDVAYEAKDVIDSIIVRDNGLL 468
Rpi-blb2        IALIKEQIGLVKEDLEFIRSFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL 478
                *:****:* **.::*:****** :  *******:* ************************

Mi1.1           HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKITVGFEEE 527
Mi1.2           HLIFSLPITIKKIKLIKEEISALDENIPKDRGLIVVNSPKKPVERKSLTTDKIIVGFEEE 528
Rpi-blb2        HLIFSLPITRKKMMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGEE 538
                ********* **: *****:* *.***.*:************** ******** *** **

Mi1.1           TNLILRKLTSGSADLDVISITGMPGSGKTTLAYKVYNDKSVSSRFDLRAWCTVDQGCDEK 587
Mi1.2           TNLILRKLTSGPADLDVISITGMPGSGKTTLAYKVYNDKSVSRHFDLRAWCTVDQGYDDK 588
Rpi-blb2        TNLILRKLTSGPADLDVISIIGMPGLGKTTLAYKVYNDKSVSSHFDLRAWCTVDQVYDEK 598
                **********.******** **** ********************:***********  *:*

Mi1.1           KLLNTIFSQVSDSDSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTWDELTRPFPESK 647
Mi1.2           KLLDTIFSQVSGSDSNLSENIDVADKLRKQLFGKRYLIVLDDVWDTTTLDELTRPFPEAK 648
Rpi-blb2        KLLDKIFNQVSDSNSKLSENIDVADKLRKQLFGKRYLIVLDDVWDTNTWDELTRPFPDGM 658
                ***:.**.***.*:*:*********************************.* ********:.

Mi1.1           KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLEKRAFGNESCPDELLDVGKEI 707
Mi1.2           KGSRIILTTREKEVALHGKLNTDPLDLRLLRPDESWELLDKRTFGNESCPDELLDVGKEI 708
Rpi-blb2        KGSRIILTTREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCPDELLDVGKEI 718
                ************:******* ****:*****.:******:**:*****************

Mi1.1           AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH 767
Mi1.2           AENCKGLPLVADLIAGVIAGREKKRSVWLEVQSSLSSFILNSEVEVMKVIELSYDHLPHH 768
Rpi-blb2        AENCKGLPLVVDLIAGIIAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH 778
```

```
                ********** .*****:*******:****** ..* ****:.*********:******.*

Mi1.1           LKPCLLYFASFPKDTSLTIYELNVYFGAEGFVGKTEMNSMEEVVKIYMDDLIYSSLVICF 827
Mi1.2           LKPCLLHFASWPKDTPLTIYLFTVYLGAEGFVEKTEMKGIEEVVKIYMDDLISSSLVICF 828
Rpi-blb2        LKPCLLYFASAPKDWVTTIHELKLIWGFEGFVEKTDMKSLEEVVKIYLDDLISSSLVICF 838
                ******:*** ***   **: :.:  * **** **:*:.:*******:**** *******

Mi1.1           NEIGYALNFQIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPRQITIDCDEEE-HFGLNF 886
Mi1.2           NEIGDILNFQIHDLVHDFCLIKARKENLFDRIRSSAPSDLLPRQITIDYDEEEEHFGLNF 888
Rpi-blb2        NEIGDYPTCQLHDLVHDFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNF 898
                ****   . *:***************:* *:* ***********:** *::* ******

Mi1.1           VMFDSNKKRHSGKHLYSLRIIGDQLDDSVSDAFHLRHLRLLRVLDLHTSFIMVKDSLLNE 946
Mi1.2           VMFDSNKKRHSGKHLYSLRINGDQLDDSVSDAFHLRHLRLIRVLDLEPSLIMVNDSLLNE 948
Rpi-blb2        VLFGSNKKRHSGKHLYSLTINGDELDDHLSDTFHLRHLRLLRTLHLESSFIMVKDSLLNE 958
                *:*.************** * **:*** :**:********:*.*.*..*:***:******

Mi1.1           ICMLNHLRYLSIDTQVKYLPLSFSNLWNLESLFVSTNRSILVLLPRILDLVKLRVLSVDA 1006
Mi1.2           ICMLNHLRYLRIRTQVKYLPFSFSNLWNLESLFVSNKGSILVLLPRILDLVKLRVLSVGA 1008
Rpi-blb2        ICMLNHLRYLSIGTEVKSLPLSFSNLWNLEILFVDNKESTLILLPRIWDLVKLQVLFTTA 1018
                ********** * *:** **:********* ***..: * *:***** *****:** . *

Mi1.1           CSFFDMDADESILIAEDTKLENLRILTELLISYSKDTKNIFKRFPNLQLLSFELKESWDY 1066
Mi1.2           CSFFDMDADESILIAKDTKLENLRILGELLISYSKDTMNIFKRFPNLQVLQFELKESWDY 1068
Rpi-blb2        CSFFDMDADESILIAEDTKLENLTALGELVLSYWKDTEDIFKRLPNLQVLHFKLKESWDY 1078
                ***************:*******  * **::** *** :****:****:* *:*******

Mi1.1           STEQRWFSELDFLTELETLSVGFKSSNTNDSGSSVATNRPWDFHFPSNLKILWLREFPLT 1126
Mi1.2           STEQHWFPKLDCLTELETLCVGFKSSNTNHCGSSVVTNRPWDFHFPSNLKELLLYDFPLT 1128
Rpi-blb2        STEQYWFPKLDFLTELEKLTVDFERSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT 1138
                ****:**.:** *****.* *.*: ****..***.. **********.** * * :****
```

```
Mi1.1           SDSLSTIARLPNLEELSLYHTIIHGEEWNMGEEDTFENLKFLNFNQVSISKWEVGEESFP 1186
Mi1.2           SDSLSTIARLPNLENLSLYDTIIQGEEWNMGEEDTFENLKFLNLRLLTLSKWEVGEESFP 1188
Rpi-blb2        SDSLSTIARLLNLEELYLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP 1198
                ********** ***:* ** ***:**************** * :  : :***********

Mi1.1           NLEKLKLRGCHKLEEIPPSFGDIYSLKSIKIVKSPQLEDSALKIKEYAEDMRGGDELQIL 1246
Mi1.2           NLEKLKLQECGKLEEIPPSFGDIYSLKFIKIVKSPQLEDSALKIKKYAEDMRGGNDLQIL 1248
Rpi-blb2        TLEKLELSDCHNLEEIPSSFGDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL 1258
                .****:*  * :*****.********* *::*:*****:******:********::****

Mi1.1           GQKNIPLFK 1255
Mi1.2           GQKNIPLFK 1257
Rpi-blb2        GQKDIPLFK 1267
                ***:*****
```

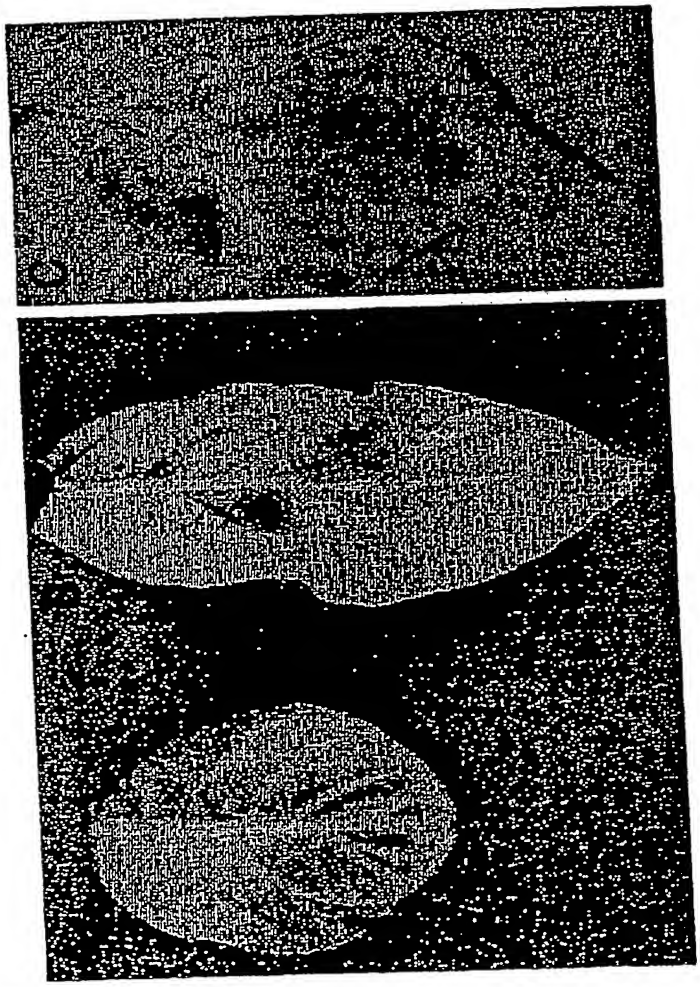


Figure 18